Implementation of an individual-based model for microbial colony dynamics

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OBJECTIVE(S)

Traditionally, mathematical models in predictive microbiology are set up as low-complexity systems of coupled differential and/or algebraic equations that express the dynamics of macroscopic characteristics of the integral microbial population (e.g., global cell density). These models are accurately applicable to describe the planktonic dynamics of pure cultures with a relatively high cell number in homogeneous liquids. For this reason and because of their low complexity, macroscopic models are frequently applied in food industry. However, most food products consist of a structured medium that restricts microbial mobility. According to this restriction, microorganisms grow locally in dense colonies. The relatively high cell number in these colonies causes nutrient overconsumption and overproduction of acid metabolites. Consequently, nutrient depletion and acidification occur in the colony center. This implies that the cells exhibit strongly different individual behavior according to their position along the colony radius. As a consequence, the traditional macroscopic models that consider the global dynamics of a population of similarly behaving organisms are not appropriate to predict microbial dynamics in structured media.

METHOD(S)

In order to take into account the different individual behavior of microorganisms in a colony, the colony dynamics are modeled by means of an individual-based model. In this individual-based model, the individual cell is considered as the modeling unit instead of the global population. This implies that the global colony dynamics are not modeled explicitly, but emerge from sub-processes at the microscopic level. These sub-processes include (i) the individual behavior of the cells (i.e., growth, reproduction and survival in stressful conditions), (ii) interaction of the microorganisms with the medium (i.e., substrate uptake and metabolite excretion), (iii) mutual interactions between cells (i.e., avoiding spatial overlap) and (iv) transport processes in the medium (i.e., diffusion of nutrients and metabolites). As a case study, colony dynamics of Escherichia coli K-12 MG1655 in BHI-impregnated gelatin are considered. During the last decade, many experimental data about this E. coli strain have been obtained at BioTeC. Several software toolkits provide an easy-to-use framework to implement the individual-based model. As mature colonies contain millions of cells, special attention is paid to simulation run times. For this reason, the Repast Simphony software toolkit is selected. In addition, only a two-dimensional layer of cells is simulated. Diffusion processes are modeled by means of an ADI scheme that is implemented with the computationally efficient Thomas algorithm.

RESULTS

From the simulations with the individual-based model, typical colony behavior emerges, e.g., a linear increase of the colony radius in case of diffusion-limited colony growth1. Varying the diffusion coefficient or initial concentration of the nutrient implies changes in the colony morphology, which

is in accordance to previously obtained experimental data2 and simulations3. Due to nutrient deprivation and acidification of the colony center, a central zone of inactivated cells emerges.

CONCLUSIONS AND IMPACT OF THE STUDY

Traditionally, models in predictive microbiology describe macroscopic characteristics of an integral microbial population with similarly behaving microorganisms in homogeneous liquid media. In order to relieve the inaccuracies of these models in predicting microbial dynamics in structured food media, an individual-based model has been implemented in the easy-to-use software framework Repast Simphony. On the long term, the information that will be generated with the individual-based model will be incorporated in the mathematical structure of the classical macroscopic predictive models. In this way, a low-complexity but more accurate model suitable for industry purposes will be created to describe microbial population dynamics in structured food media.

REFERENCES

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